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09/481990
1-11-00
B-60

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Art Unit :
Examiner :
Serial No. : Not yet known
Filed : January 11, 2000
Inventor : Florian Lesage, et al.

09/481990
AU 1842

1600 Market Street
Suite 3600
Philadelphia, PA 19103
Docket: 989.6351DIV

Title : Family of Mammalian Potassium Channels, Their Cloning And
: Their Use, Especially For The Screening of Drugs

CI 435

Dated: January 11, 2000

REQUEST TO USE COMPUTER READABLE FORM FROM
ANOTHER APPLICATION UNDER 37 C.F.R. §1.821(E)

Box Patent Application
Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

The computer readable Nucleotide Sequence and/or Amino Acid Sequence Disclosure in this divisional application is identical with that filed in parent application Serial No. 08/749,816, filed November 15, 1996. In accordance with 37 CFR 1.821(e), please use the last-filed computer readable form filed in that application as the computer readable form for the instant application. It is understood that the Patent and Trademark Office will make the necessary change in application number and filing date for the computer readable form that will be used for the instant application. A paper copy of the Sequence Listing is included in a separately filed preliminary amendment for incorporation into the specification, filed with this statement.

We submit that no fee is due. If, however, it is deemed that a fee is required, the Commissioner is authorized to charge Deposit Account 13-3405. This authorization is made in duplicate.

Respectfully submitted,

Gerard J. Weiser

Gerard J. Weiser
Reg. No. 19,763
SCHNADER HARRISON SEGAL & LEWIS LLP
Attorneys for Applicants

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/481,990DATE: 06/20/2000
TIME: 03:23:38

INPUT SET: S35645.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Lesage, Florian
Guillemare, Eric
Fink, Michel
Duprat, Fabrice
Lazdunki, Michel
Romey, Georges
Barhanin, Jacques

ENTERED

(ii) TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
OF DRUGS

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: WEISER & ASSOCIATES
(B) STREET: 230 South Fifteenth Street, Suite 500
(C) CITY: Philadelphia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19102

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/481,990
(B) FILING DATE: 11-JAN-2000
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/749,816
(B) FILING DATE: 15-NOV-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Weiser, Gerard J.
(B) REGISTRATION NUMBER: 19,763
(C) REFERENCE/DOCKET NUMBER: 989.6351P

RAW SEQUENCE LISTING PATENT APPLICATION US/09/481,990

DATE: 06/20/2000
TIME: 03:23:39

INPUT SET: S35645.raw

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47      (ix) TELECOMMUNICATION INFORMATION:
48          (A) TELEPHONE: 215-875-8383
49          (B) TELEFAX: 215-875-8394
50
51
52      (2) INFORMATION FOR SEQ ID NO:1:
53
54          (i) SEQUENCE CHARACTERISTICS:
55              (A) LENGTH: 1894 base pairs
56              (B) TYPE: nucleic acid
57              (C) STRANDEDNESS: single
58              (D) TOPOLOGY: linear
59
60          (ii) MOLECULE TYPE: cDNA
61
62
63          (ix) FEATURE:
64              (A) NAME/KEY: CDS
65              (B) LOCATION: 183..1190
66
67
68          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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70      GGGCAGGAAG ACGGCGCTGC CCGGAGGAGC GGGGCGGGCG GGCGCGCGGG GGAGCGGGCG      60
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72      GCGGGCGGGA GCCAGGCCCG GCGGGGGGCG GGGGCGGCGG GGCCAGAAGA GGCGGCGGGC      120
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74      CGCGCTCCGG CCGGTCTGCG GCGTTGGCCT TGGCTTTGGC TTTGGCGGCG GCGGTGGAGA      180
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76      AG ATG CTG CAG TCC CTG GCC GGC AGC TCG TGC GTG CGC CTG GTG GAG      227
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78      1          5          10          15
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80      CGG CAC CGC TCG GCC TGG TGC TTC GGC TTC CTG GTG CTG GGC TAC TTG      275
81      Arg His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu
82      20          25          30
83
84      CTC TAC CTG GTC TTC GGC GCA GTG GTC TTC TCC TCG GTG GAG CTG CCC      323
85      Leu Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro
86      35          40          45
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88      TAT GAG GAC CTG CTG CGC CAG GAG CTG CGC AAG CTG AAG CGA CGC TTC      371
89      Tyr Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe
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92      TTG GAG GAG CAC GAG TGC CTG TCT GAG CAG CAG CTG GAG CAG TTC CTG      419
93      Leu Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu
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96      GGC CGG GTG CTG GAG GCC AGC AAC TAC GGC GTG TCG GTG CTC AGC AAC      467
97      Gly Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn
98      80          85          90          95
99

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/481,990

DATE: 06/20/2000
TIME: 03:23:40

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104	AGC ACC GTG CTC TCC ACC ACA GGT TAT GGC CAC ACC GTG CCC TTG TCA	563
105	Ser Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser	
106	115 120 125	
107		
108	GAT GGA GGT AAG GCC TTC TGC ATC ATC TAC TCC GTC ATT GGC ATT CCC	611
109	Asp Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro	
110	130 135 140	
111		
112	TTC ACC CTC CTG TTC CTG ACG GCT GTG GTC CAG CGC ATC ACC GTG CAC	659
113	Phe Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His	
114	145 150 155	
115		
116	GTC ACC CGC AGG CCG GTC CTC TAC TTC CAC ATC CGC TGG GGC TTC TCC	707
117	Val Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser	
118	160 165 170 175	
119		
120	AAG CAG GTG GTG GCC ATC GTC CAT GCC GTG CTC CTT GGG TTT GTC ACT	755
121	Lys Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr	
122	180 185 190	
123		
124	GTG TCC TGC TTC TTC TTC ATC CCG GCC GCT GTC TTC TCA GTC CTG GAG	803
125	Val Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu	
126	195 200 205	
127		
128	GAT GAC TGG AAC TTC CTG GAA TCC TTT TAT TTT TGT TTT ATT TCC CTG	851
129	Asp Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu	
130	210 215 220	
131		
132	AGC ACC ATT GGC CTG GGG GAT TAT GTG CCT GGG GAA GGC TAC AAT CAA	899
133	Ser Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln	
134	225 230 235	
135		
136	AAA TTC AGA GAG CTC TAT AAG ATT GGG ATC ACG TGT TAC CTG CTA CTT	947
137	Lys Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu	
138	240 245 250 255	
139		
140	GGC CTT ATT GCC ATG TTG GTA GTT CTG GAA ACC TTC TGT GAA CTC CAT	995
141	Gly Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His	
142	260 265 270	
143		
144	GAG CTG AAA AAA TTC AGA AAA ATG TTC TAT GTG AAG AAG GAC AAG GAC	1043
145	Glu Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp	
146	275 280 285	
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148	GAG GAT CAG GTG CAC ATC ATA GAG CAT GAC CAA CTG TCC TTC TCC TCG	1091
149	Glu Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser	
150	290 295 300	
151		
152	ATC ACA GAC CAG GCA GCT GGC ATG AAA GAG GAC CAG AAG CAA AAT GAG	1139

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153	Ile Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu	
154	305 310 315	
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156	CCT TTT GTG GCC ACC CAG TCA TCT GCC TGC GTG GAT GGC CCT GCA AAC	1187
157	Pro Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn	
158	320 325 330 335	
159		
160	CAT TGAGCGTAGG ATTTGTTGCA TTATGCTAGA GCACCAGGGT CAGGGTGCAA	1240
161	His	
162		
163		
164	GGAAGAGGCT TAAGTATGTT CATTTTTTATC AGAATGCAAA AGCGAAAATT ATGTCACTTT	1300
165		
166	AAGAAATAGC TACTGTTTGC AATGTCTTAT TAAAAAACAA CAAAAAAGA CACATGGAAC	1360
167		
168	AAAGAAGCTG TGACCCCAGC AGGATGTCTA ATATGTGAGG AAATGAGATG TCCACCTAAA	1420
169		
170	ATTCATATGT GACAAAATTA TCTCGACCTT ACATAGGAGG AGAATACTTG AAGCAGTATG	1480
171		
172	CTGCTGTGGT TAGAAGCAGA TTTTATACTT TTAActGGAA ACTTTGGGGT TTGCATTTAG	1540
173		
174	ATCATTTAGC TGATGGCTAA ATAGCAAAAT TTATATTTAG AAGCAAAAAA AAAAAGCATA	1600
175		
176	GAGATGTGTT TTATAAATAG GTTTATGTGT ACTGGTTTGC ATGTACCCAC CAAAATGAT	1660
177		
178	TATTTTTTGA GAATCTAAGT CAAACTCACT ATTTATAATG CATAGGTAAC CATTAACTAT	1720
179		
180	GTACATATAA AGTATAAATA TGTTTATATT CTGTACATAT GGTTTAGGTC ACCAGATCCT	1780
181		
182	AGTGTAGTTC TGAAACTAAG ACTATAGATA TTTTGTCTTCT TTTGATTTCT CTTTATACTA	1840
183		
184	AAGAATCCAG AGTTGCTACA ATAAAAATAAG GGAATAATA AAAAAAAAAA AAAA	1894

(2) INFORMATION FOR SEO ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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198 Met Leu Gln Ser Leu Ala Gly Ser Ser Cys Val Arg Leu Val Glu Arg
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201 His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu Leu
202      20                      25              30
203
204 Tyr Leu Val Phe Gly Ala Val Val Phe Ser Ser Val Glu Leu Pro Tyr
205      35                      40              45

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RAW SEQUENCE LISTING PATENT APPLICATION US/09/481,990

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206
207   Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe Leu
208       50                      55                      60
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210   Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly
211       65                      70                      75                      80
212
213   Arg Val Leu Glu Ala Ser Asn Tyr Gly Val Ser Val Leu Ser Asn Ala
214               85                      90                      95
215
216   Ser Gly Asn Trp Asn Trp Asp Phe Thr Ser Ala Leu Phe Phe Ala Ser
217               100                      105                      110
218
219   Thr Val Leu Ser Thr Thr Gly Tyr Gly His Thr Val Pro Leu Ser Asp
220               115                      120                      125
221
222   Gly Gly Lys Ala Phe Cys Ile Ile Tyr Ser Val Ile Gly Ile Pro Phe
223       130                      135                      140
224
225   Thr Leu Leu Phe Leu Thr Ala Val Val Gln Arg Ile Thr Val His Val
226       145                      150                      155                      160
227
228   Thr Arg Arg Pro Val Leu Tyr Phe His Ile Arg Trp Gly Phe Ser Lys
229               165                      170                      175
230
231   Gln Val Val Ala Ile Val His Ala Val Leu Leu Gly Phe Val Thr Val
232               180                      185                      190
233
234   Ser Cys Phe Phe Phe Ile Pro Ala Ala Val Phe Ser Val Leu Glu Asp
235               195                      200                      205
236
237   Asp Trp Asn Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser
238       210                      215                      220
239
240   Thr Ile Gly Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn Gln Lys
241       225                      230                      235                      240
242
243   Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu Gly
244               245                      250                      255
245
246   Leu Ile Ala Met Leu Val Val Leu Glu Thr Phe Cys Glu Leu His Glu
247               260                      265                      270
248
249   Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp Glu
250               275                      280                      285
251
252   Asp Gln Val His Ile Ile Glu His Asp Gln Leu Ser Phe Ser Ser Ile
253       290                      295                      300
254
255   Thr Asp Gln Ala Ala Gly Met Lys Glu Asp Gln Lys Gln Asn Glu Pro
256       305                      310                      315                      320
257
258   Phe Val Ala Thr Gln Ser Ser Ala Cys Val Asp Gly Pro Ala Asn His

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/481,990

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Original Text

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/09/481,990

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PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/481,990

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TIME: 03:23:44

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